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Meeting Background and Purpose

This meeting provides an opportunity for the Medicare Advisory Panel on Clinical Diagnostic Laboratory Tests (the CDLT Panel) to publicly convene and make recommendations to the Secretary of the Department of Health and Services and the Administrator of CMS regarding crosswalking and gapfilling for new and reconsidered laboratory tests discussed during the CLFS Annual Public Meeting for CY 2023. The CDLT Panel may also provide input on any other CY 2023 CLFS issues that are designated in the Panel's charter and specified in this agenda. Notice of this meeting and additional supplemental information regarding the CDLT Panel were published in the Federal Register on April 18, 2022 (CMS-1777-N; 87 FR 22895).

Meeting Format

- The CDLT Panel Chair will direct the presentation and discussion of each laboratory test code on the agenda.
- Each laboratory test code under consideration will be introduced and discussed by the CDLT Panel. The focus of discussion is payment of the laboratory test code either through crosswalking the laboratory test code to another existing laboratory test code on the CLFS, or to use the gapfill methodology to determine payment. During the discussion the CDLT Panel and CMS staff may ask questions of the representative of laboratory that owns the test. Once CDLT Panel discussions are concluded, the suggestions from the Panel are summarized and the Panel votes on their recommendation for payment.
- The meeting is divided into two sessions, one session on each date of the meeting. Session times are approximate and subject to change.

Meeting Connection Instructions and Details

- <u>Listen-in via audio and watch via Zoom connection only</u> details are provided using instructions described in Appendix 1.
- Please note that the video or audio recordings of the meeting will not be immediately available after the conclusion of the meeting.

AGENDA

Monday July 18, 2022

| Time | Topic | Supporting Resource |
|-------------|--|------------------------|
| 8:30 a.m. | Check-In and Audio/Video Connection Test Check | Resource |
| 9:00 a.m. | Welcome and Panel Introductions: Karen Nakano, M.D., Panel Chair, CMS Physician and Rasheeda Arthur, PhD, Panel Designated Federal Officer | |
| 9:15 -12:00 | Session 1: | Appendix 3 |
| p.m. | I. Chemistry II. Genomic Sequencing Related Tests III. Microbiology | |
| 12:00- | Lunch Break | |
| 1:00pm | Please Note: All speakers please reconnect by 12:45pm | |
| 1:00-4:30 | Session 1: (continued): | Appendix 3 |
| p.m. | I. Chemistry | |
| | II. Genomic Sequencing Related Tests | |
| | III. Microbiology | |
| 4:30 p.m. | Meeting Adjourns | |

Tuesday July 19, 2022

| Time | Topic | Supporting | | | | | | |
|-------------|---|------------|--|--|--|--|--|--|
| - | Tr. | Resource | | | | | | |
| 8:30 a.m. | Check-In and Audio/Video Connection Test Check | | | | | | | |
| 9:00 a.m. | Reconvene Meeting: Karen Nakano, M.D., | | | | | | | |
| | Panel Chair, CMS Physician | | | | | | | |
| 9:15 -12:00 | Session 2: | Appendix 4 | | | | | | |
| p.m. | IV. Hematology and Coagulation | | | | | | | |
| - | V. Tests with algorithm in code descriptor to report | | | | | | | |
| | risk/likelihood/predictive score | | | | | | | |
| | VI. Immunology | | | | | | | |
| 12:00- | Lunch Break | | | | | | | |
| 1:00pm | Please Note: All speakers please reconnect by 12:45pm | | | | | | | |
| 1:00-4:30 | Session 2: (continued): | Appendix 4 | | | | | | |
| p.m. | IV. Hematology and Coagulation | | | | | | | |
| | V. Tests with algorithm in code descriptor to report | | | | | | | |
| | risk/likelihood/predictive score | | | | | | | |
| | VI. Immunology | | | | | | | |
| 4:30 p.m. | Meeting Adjourns | | | | | | | |

^{***}Please note that the order of the agenda and content of the appendices are subject to change.***

Appendix 1: Audio and/or Video Access: Join the meeting by Zoom

Please click the link below to join the webinar:

https://cms.zoomgov.com/webinar/register/WN UGnBlaA3SUWVj5y ZclGt Q

Webinar ID: 161 798 0314

Password: 709448

US: +1 669 254 5252 or +1 646 828 7666 or 833 568 8864 (Toll Free)

Appendix 2: Access to CLFS CY 2023 New and Reconsidered Codes and Other Information

 For a list of <u>CY 2023 new and reconsidered codes</u> that will be discussed during the CDLT Panel meeting, please go to the CLFS Annual Laboratory Meeting website at: https://www.cms.gov/Medicare/Medicare-Fee-for-Service-Payment/ClinicalLabFeeSched/Laboratory Public Meetings

Scroll down to "Test Code Updates" for access to the CY 2023 new and reconsidered code list.

- For <u>CLFS Annual Laboratory Public meeting agenda</u> from June 23, 2022 please see: https://www.cms.gov/files/document/agenda-clfs-annual-laboratory-meeting-june-23-2022.pdf
- 3. For a recording of the CFLS Annual Laboratory Public Meeting from June 23, 2022, please see links below:
 - a. Part I:

https://cms.zoomgov.com/rec/play/vlFecgQcw7yNODq7QlMmmTNvhoWerjU3JYWY_Y3L5ouc4ITj1tvfR76El42A1OGubJsaIuI8_aZgB9VH.7QsML2bLJBxxhg 0g

Passcode: nd0?5!5j

b. Part II:

https://cms.zoomgov.com/rec/play/w8uTb3BRZlftdglD82moFjTCI9nUaf6fk0GV 0f8b157HzE9DIIkwys46ka-cbeQZ2PQmqvL1_IRoB-0G.QBNyvw-bzEvHTWTg Passcode: nd0?5!5j

4. For a copy of <u>CY 2022 - Clinical Laboratory Fee Schedule Test Codes Final Payment</u>

<u>Determinations</u> that were discussed during last year's CLFS Annual Laboratory Meeting and the Medicare Advisory Panel for Clinical Diagnostic Laboratory Tests (CDLT Panel) Meeting, please see link: https://www.cms.gov/files/zip/cy2022-clfs-test-codes-final-payment-determinations.zip

Appendix 3: Session 1 – July 18, 2022 Summary of codes

Corrections to order of codes:

- a. Item #32 code 81445 was moved to follow item #30 code 0022U.
- b. Item #98 code 86364 was moved to follow item #95 code 86258
- c. Item #102 code 87548 was moved to follow item #105 code 0x56U

| FACA Panel Item # | ALM Item # | Subcomm ittee | Code # | Code Type | Slide category | Long Code Descriptor |
|-------------------------|------------------|------------------|--------|-----------------|--|---|
| 1 | 75 | CHIM | 84XXX | NEW | Chemistry | Thiopurine S-methyltransferase (TPMT) |
| 2 | 39 | CHIM | 80220 | Reconsideration | Chemistry | Hydroxychloroquine |
| 3 | 41 | CHIM | 83529 | Reconsideration | Chemistry | Interleukin-6 (IL-6) |
| 4 | 96 | СНІМ | 0X46U | PLA | Chemistry | Hepatology (nonalcoholic fatty liver disease [NAFLD]), semiquantitative evaluation of 28 lipid markers by liquid chromatography with tandem mass spectrometry (LC-MS/MS), serum, reported as at-risk for nonalcoholic steatohepatitis (NASH) or not NASH |
| 5 | 98 | CHIM | 0X48U | PLA | Chemistry | Beta amyloid, Aβ40 and Aβ42 by liquid chromatography with tandem mass spectrometry (LC-MS/MS), ratio, plasma |
| 6 | 14 | MoG | 0298U | PLA | Genomic Sequencing Related Tests WHOLE GENOME; Drug metabolism pharmacogenomics/pharmacoge netics | Oncology (pan tumor), whole transcriptome sequencing of paired malignant and normal RNA specimens, fresh or formalin-fixed paraffin-embedded (FFPE) tissue, blood or bone marrow, comparative sequence analyses and expression level and chimeric transcript identification |
| 7 | 13 | MoG | 0297U | PLA | Genomic Sequencing Related Tests WHOLE GENOME; Drug metabolism pharmacogenomics/pharmacoge netics | Oncology (pan tumor), whole genome sequencing of paired malignant and normal DNA specimens, fresh or formalin fixed paraffin-embedded (FFPE) tissue, blood or bone marrow, comparative sequence analyses and variant identification |
| 8 | 15 | MoG | 0299U | PLA | Genomic Sequencing Related Tests WHOLE GENOME; Drug metabolism pharmacogenomics/pharmacoge netics | Oncology (pan tumor), whole genome optical genome mapping of paired malignant and normal DNA specimens, fresh frozen tissue, blood, or bone marrow, comparative structural variant identification |
| 9 | 16 | MoG | 0300U | PLA | G Genomic Sequencing Related Tests | Oncology (pan tumor), whole genome sequencing and optical genome mapping of paired malignant and normal DNA specimens, fresh tissue, blood, or bone marrow, comparative sequence analyses and variant identification |

| FACA Panel Item # | ALM Item # | Subcomm ittee | Code # | Code Type | Slide category | Long Code Descriptor |
|-------------------------|------------------|------------------|--------|-----------|---|--|
| | | | | | WHOLE GENOME; Drug metabolism pharmacogenomics/pharmacoge netics | |
| 10 | 70 | MoG | 8X000 | NEW | Genomic Sequencing Related Tests WHOLE GENOME; Drug metabolism pharmacogenomics/pharmacoge netics | Drug metabolism (eg, pharmacogenomics) genomic sequence analysis panel, must include testing of at least 6 genes, including CYP2C19, CYP2D6, and CYP2D6 duplication/deletion analysis |
| 11 | 95 | MoG | 0X45U | PLA | Genomic Sequencing Related Tests TARGETED; Drug metabolism pharmacogenomics/pharmacoge netics | Drug metabolism or processing (multiple conditions), whole blood or buccal specimen, DNA analysis, 27 gene report, with variant analysis including reported phenotypes and impacted gene-drug interactions |
| 12 | 97 | MoG | 0X47U | PLA | Genomic Sequencing Related Tests TARGETED; Drug metabolism pharmacogenomics/pharmacoge netics | Psychiatry (eg, depression, anxiety, attention deficit hyperactivity disorder [ADHD]), genomic analysis panel, variant analysis of 15 genes, including deletion/duplication analysis of CYP2D6 |
| 13 | 99 | MoG | 0X50U | PLA | Genomic Sequencing Related Tests TARGETED; Drug metabolism pharmacogenomics/pharmacoge netics | Drug metabolism or processing (multiple conditions), whole blood or buccal specimen, DNA analysis, 25 gene report, with variant analysis and reported phenotypes |
| 14 | 100 | MoG | 0X51U | PLA | Genomic Sequencing Related Tests TARGETED; Drug metabolism pharmacogenomics/pharmacoge netics | Drug metabolism or processing (multiple conditions), whole blood or buccal specimen, DNA analysis, 16 gene report, with variant analysis and reported phenotypes |
| 15 | 101 | MoG | 0X52U | PLA | Genomic Sequencing Related Tests TARGETED; Drug metabolism pharmacogenomics/pharmacoge netics | Drug metabolism or processing (multiple conditions), whole blood or buccal specimen, DNA analysis, 27 gene report, with variant analysis and reported phenotypes |
| 16 | 2 | MoG | 0286U | PLA | Genomic Sequencing Related Tests TARGETED; Drug metabolism pharmacogenomics/pharmacoge netics | CEP72 (centrosomal protein, 72-KDa), NUDT15 (nudix hydrolase 15) and TPMT (thiopurine S-methyltransferase) (eg, drug metabolism) gene analysis, common variants |

| FACA Panel Item # | ALM Item # | Subcomm ittee | Code # | Code Type | Slide category | Long Code Descriptor |
|-------------------------|------------------|------------------|--------|--|--|--|
| 17 | 67 | MoG | 0331U | PLA | Genomic Sequencing Related Tests WHOLE GENOME | Oncology (hematolymphoid neoplasia), optical genome mapping for copy number alterations and gene rearrangements utilizing DNA from blood or bone marrow, report of clinically significant alternations |
| 18 | 88 | MoG | 0X38U | PLA | Genomic Sequencing Related Tests WHOLE GENOME | Rare diseases (constitutional/heritable disorders), whole genome sequence analysis, including small sequence changes, copy number variants, deletions, duplications, mobile element insertions, uniparental disomy (UPD), inversions, aneuploidy, mitochondrial genome sequence analysis with heteroplasmy and large deletions, short tandem repeat (STR) gene expansions, blood or saliva, identification and categorization of genetic variants, each comparator genome (eg, parent) |
| 19 | 86 | MoG | 0X36U | PLA | Genomic Sequencing Related Tests WHOLE GENOME | Rare diseases (constitutional/heritable disorders), whole genome sequence analysis, including small sequence changes, copy number variants, deletions, duplications, mobile element insertions, uniparental disomy (UPD), inversions, aneuploidy, mitochondrial genome sequence analysis with heteroplasmy and large deletions, short tandem repeat (STR) gene expansions, fetal sample, identification and categorization of genetic variants |
| 20 | 91 | MoG | 0X41U | PLA | Genomic Sequencing Related Tests WHOLE GENOME | Oncology (pan-cancer), analysis of minimal residual disease (MRD) from plasma, with assays personalized to each patient based on prior next-generation sequencing of the patient's tumor and germline DNA, reported as absence or presence of MRD, with disease-burden correlation, if appropriate |
| 21 | 22 | MoG | 0306U | PLA | Genomic Sequencing Related Tests TARGETED; cell free DNA | Oncology (minimal residual disease [MRD]), next-generation targeted sequencing analysis, cell-free DNA, initial (baseline) assessment to determine a patient-specific panel for future comparisons to evaluate for MRD (Do not report 0306U in conjunction with 0307U) |
| 22 | 23 | MoG | 0307U | PLA | Genomic Sequencing Related Tests TARGETED; cell free DNA | Oncology (minimal residual disease [MRD]), next-generation targeted sequencing analysis of a patient-specific panel, cell-free DNA, subsequent assessment with comparison to previously analyzed patient specimens to evaluate for MRD (Do not report 0307U in conjunction with 0306U) |
| 23 | 34 | MoG | 0318U | PLA | Genomic Sequencing Related Tests TARGETED; METHYLATION ANALYSIS | Pediatrics (congenital epigenetic disorders), whole genome methylation analysis by microarray for 50 or more genes, blood |
| 24 | 57 | MoG | 0229U | Reconsideration/ Substantially Revised | Genomic Sequencing Related Tests TARGETED; METHYLATION ANALYSIS | BCAT1 (Branched chain amino acid transaminase 1) and IKZF1 (IKAROS family zinc finger 1) (eg, colorectal cancer) promoter methylation analysis |
| 25 | 40 | MoG | 81349 | Reconsideration | Genomic Sequencing Related Tests TARGETED; CHROMOSOME | Cytogenomic (genome-wide) analysis for constitutional chromosomal abnormalities; interrogation of genomic regions for copy number and loss-of-heterozygosity variants, low-pass sequencing analysis |

| FACA Panel Item # | ALM Item # | Subcomm ittee | Code # | Code Type | Slide category | Long Code Descriptor |
|-------------------------|------------------|------------------|--------|-----------------|---|--|
| 26 | 92 | MoG | 0X42U | PLA | Genomic Sequencing Related Tests TARGETED; CHROMOSOME | Fetal aneuploidy DNA sequencing comparative analysis, fetal DNA from products of conception, reported as normal (euploidy), monosomy, trisomy, or partial deletion/duplication, mosaicism, and segmental aneuploid |
| 27 | 71 | MoG | 814XX | NEW | Genomic Sequencing Related Tests TARGETED | Inherited bone marrow failure syndromes (IBMFS) (eg, Fanconi anemia, dyskeratosis congenita, Diamond-Blackfan anemia, Shwachman-Diamond syndrome, GATA2 deficiency syndrome, congenital amegakaryocytic thrombocytopenia) sequence analysis panel, must include sequencing of at least 30 genes, including BRCA2, BRIP1, DKC1, FANCA, FANCB, FANCC, FANCD2, FANCE, FANCF, FANCG, FANCI, FANCL, GATA1, GATA2, MPL, NHP2, NOP10, PALB2, RAD51C, RPL11, RPL35A, RPL5, RPS10, RPS19, RPS24, RPS26, RPS7, SBDS, TERT, and TINF2 |
| 28 | 85 | MoG | 0X35U | PLA | Genomic Sequencing Related Tests TARGETED; VARIANTS, REARRANGEMENTS, MICROSATELLITE INSTABILITY | Oncology (solid organ), targeted genomic sequence analysis, formalin-fixed paraffin-embedded (FFPE) tumor tissue, DNA analysis, 84 or more genes, interrogation for sequence variants, gene copy number amplifications, gene rearrangements, microsatellite instability and tumor mutational burden |
| 29 | 82 | MoG | 0276U | Revision | Genomic Sequencing Related Tests TARGETED | Hematology (inherited thrombocytopenia), genomic sequence analysis of 42 genes, blood, buccal swab, or amniotic fluid |
| 30 | 69 | MoG | 0022U | Reconsideration | Genomic Sequencing Related Tests TARGETED; VARIANTS; DNA and RNA | Targeted genomic sequence analysis panel, cholangiocarcinoma and non-small cell lung neoplasia, DNA and RNA analysis, 1-23 genes, interrogation for sequence variants and rearrangements, reported as presence/absence of variants and associated therapy(ies) to consider |
| 32 | 76 | MoG | 81445 | NEW | Genomic Sequencing Related Tests TARGETED; VARIANTS, REARRANGEMENTS | Targeted genomic sequence analysis panel, solid organ neoplasm, 5-50 genes (eg, ALK, BRAF, CDKN2A, EGFR, ERBB2, KIT, KRAS, NRAS, MET, PDGFRA, PDGFRB, PGR, PIK3CA, PTEN, RET), interrogation for sequence variants and copy number variants or rearrangements, if performed; DNA analysis or combined DNA and RNA analysis |
| 31 | 72 | MoG | 814X1 | NEW | Genomic Sequencing Related Tests TARGETED; VARIANTS, REARRANGEMENTS | Targeted genomic sequence analysis panel, solid organ neoplasm, 5-50 genes (eg, ALK, BRAF, CDKN2A, EGFR, ERBB2, KIT, KRAS, NRAS, MET, PDGFRA, PDGFRB, PGR, PIK3CA, PTEN, RET), interrogation for sequence variants and copy number variants or rearrangements, if performed; RNA analysis |
| 33 | 74 | MoG | 814X3 | NEW | Genomic Sequencing Related Tests TARGETED; VARIANTS, REARRANGEMENTS, ISOFORM or RNA EXPRESSION | Targeted genomic sequence analysis panel, solid organ or hematolymphoid neoplasm or disorder, 51 or greater genes (eg, ALK, BRAF, CDKN2A, CEBPA, DNMT3A, EGFR, ERBB2, EZH2, FLT3, IDH1, IDH2, JAK2, KIT, KRAS, MLL, NPM1, NRAS, MET, NOTCH1, PDGFRA, PDGFRB, PGR, PIK3CA, PTEN, RET), interrogation for sequence variants and copy number variants or rearrangements, or isoform expression or mRNA expression levels, if performed; RNA analysis |

| FACA Panel Item # | ALM Item # | Subcomm ittee | Code # | Code Type | Slide category | Long Code Descriptor |
|-------------------------|------------------|------------------|-----------------|-----------|---|---|
| 34 | 62 | MoG | 0326U | PLA | Genomic Sequencing Related Tests TARGETED; VARIANTS, REARRANGEMENTS, MICORSATELLITE INSTABILITY | Targeted genomic sequence analysis panel, solid organ neoplasm, cell-free circulating DNA analysis of 83 or more genes, interrogation for sequence variants, gene copy number amplifications, gene rearrangements, microsatellite instability and tumor mutational burden |
| 35 | 73 | MoG | 814X2 | NEW | Genomic Sequencing Related Tests TARGETED VARIANTS, REARRANGEMENTS, ISOFORM or RNA EXPRESSION | Targeted genomic sequence analysis panel, hematolymphoid neoplasm or disorder, 5-50 genes (eg, BRAF, CEBPA, DNMT3A, EZH2, FLT3, IDH1, IDH2, JAK2, KRAS, KIT, MLL, NRAS, NPM1, NOTCH1), interrogation for sequence variants, and copy number variants or rearrangements, or isoform expression or mRNA expression levels, if performed; RNA analysis |
| 36 | 90 | MoG | 0X40U | PLA | Genomic Sequencing Related Tests TARGETED; mRNA | Oncology (prostate), mRNA expression profiling of HOXC6 and DLX1, reverse transcription polymerase chain reaction (RT-PCR), first-void urine following digital rectal examination, algorithm reported as probability of high-grade cancer |
| 37 | 32 | CHIM | 0316U | PLA | Microbiology SINGLE PROTEIN | Borrelia burgdorferi (Lyme disease), OspA protein evaluation, urine |
| 38 | 77 | CHIM | 862XX/ 8X002 | NEW | Microbiology SINGLE IMMUNOASSAY IDENTIFICATION | Hepatitis B surface antigen (HBsAg), quantitative |
| 39 | 68 | CHIM | 879X1/ 87913 | NEW | Microbiology SINGLE GENOMIC IDENTIFICATION | Infectious agent genotype analysis by nucleic acid (DNA or RNA); severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (coronavirus disease [COVID-19]), mutation identification in targeted region(s) |
| 40 | 78 | CHIM | 87X68/ 8X009 | NEW | Microbiology SINGLE GENOMIC IDENTIFICATION | Infectious agent detection by nucleic acid (DNA or RNA); Anaplasma phagocytophilum, amplified probe technique |
| 41 | 79 | CHIM | 87X70/ 8X010 | NEW | Microbiology SINGLE GENOMIC IDENTIFICATION | Infectious agent detection by nucleic acid (DNA or RNA); Babesia microti, amplified probe technique |
| 42 | 80 | CHIM | 87X77/ 8X011 | NEW | Microbiology SINGLE GENOMIC IDENTIFICATION | Infectious agent detection by nucleic acid (DNA or RNA); Borrelia miyamotoi, amplified probe technique |
| 43 | 81 | CHIM | 87X99 8X012 | NEW | Microbiology SINGLE GENOMIC IDENTIFICATION | Infectious agent detection by nucleic acid (DNA or RNA); Ehrlichia chaffeensis, amplified probe technique |
| 44 | 27 | CHIM | 0311U | PLA | Microbiology MORPHOKINETIC CELLULAR ANALYSIS | Infectious disease (bacterial), quantitative antimicrobial susceptibility reported as phenotypic minimum inhibitory concentration (MIC)–based antimicrobial susceptibility for each organism identified |
| | | | | | | (Do not report 0311U in conjunction with 87076, 87077, 0086U) |

| FACA Panel Item # | ALM Item # | Subcomm ittee | Code # | Code Type | Slide category | Long Code Descriptor |
|-------------------------|------------------|------------------|--------|-----------|---|---|
| 45 | 17 | CHIM | 0301U | PLA | Microbiology PANEL GENOMIC IDENTIFICATION | Infectious agent detection by nucleic acid (DNA or RNA), Bartonella henselae and Bartonella quintana, droplet digital PCR (ddPCR); |
| 46 | 18 | CHIM | 0302U | PLA | Microbiology PANEL GENOMIC IDENTIFICATION | Infectious agent detection by nucleic acid (DNA or RNA), Bartonella henselae and Bartonella quintana, droplet digital PCR (ddPCR); following liquid enrichment |
| 47 | 37 | СНІМ | 0321U | PLA | Microbiology PANEL GENOMIC IDENTIFICATION | Infectious agent detection by nucleic acid (DNA or RNA), genitourinary pathogens, identification of 20 bacterial and fungal organisms and identification of 16 associated antibiotic-resistance genes, multiplex amplified probe technique |
| 48 | 59 | CHIM | 0323U | PLA | Microbiology PANEL GENOMIC IDENTIFICATION | Infectious agent detection by nucleic acid (DNA and RNA), central nervous system pathogen, metagenomic next-generation sequencing, cerebrospinal fluid (CSF), identification of pathogenic bacteria, viruses, parasites or fungi |
| 49 | 66 | CHIM | 0330U | PLA | Microbiology PANEL GENOMIC IDENTIFICATION | Infectious agent detection by nucleic acid (DNA or RNA), vaginal pathogen panel, identification of 27 organisms, amplified probe technique, vaginal swab |
| 50 | 103 | CHIM | 0X54U | PLA | Microbiology PANEL GENOMIC IDENTIFICATION | Infectious disease (bacterial vaginosis and vaginitis), multiplex amplified probe technique, for detection of bacterial vaginosis—associated bacteria (BVAB-2, Atopobium vaginae, and Megasphera type 1), algorithm reported as detected or not detected and separate detection of Candida species (C. albicans, C. tropicalis, C. parapsilosis, C. dubliniensis), Candida glabrata/Candida krusei, and trichomonas vaginalis, vaginal-fluid specimen, each result reported as detected or not detected |
| 51 | 104 | СНІМ | 0X55U | PLA | Microbiology PANEL GENOMIC IDENTIFICATION | Infectious agent detection by nucleic acid (DNA), Chlamydia trachomatis and Neisseria gonorrhoeae, multiplex amplified probe technique, urine, vaginal, pharyngeal, or rectal, each pathogen reported as detected or not detected |

Appendix 4: Session 2 – July 19, 2022 Summary of codes

Corrections to order of codes:

- a. Item #32 code 81445 was moved to follow item #30 code 0022U.
- b. Item #98 code 86364 was moved to follow item #95 code 86258
- c. Item #102 code 87548 was moved to follow item #105 code 0x56U

| FACA Panel | ALM Item | Subcommittee | Code # | Code Type | Slide category | Long Code Descriptor |
|---------------|-------------|--------------|--------|-----------|---|---|
| Item # | # | | | | | |
| 52 | 19 | CHIM | 0303U | PLA | Hematology and Coagulation | Hematology, red blood cell (RBC) adhesion to endothelial/subendothelial adhesion molecules, functional assessment, whole blood, with algorithmic analysis and result reported as an RBC adhesion index; hypoxic |
| 53 | 20 | CHIM | 0304U | PLA | Hematology and Coagulation | Hematology, red blood cell (RBC) adhesion to endothelial/subendothelial adhesion molecules, functional assessment, whole blood, with algorithmic analysis and result reported as an RBC adhesion index; normocytic |
| 54 | 21 | CHIM | 0305U | PLA | Hematology and Coagulation | Hematology, red blood cell (RBC) functionality and deformity as a function of shear stress, whole blood, reported as a maximum elongation index |
| 55 | 1 | MoG | 0285U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score CELL FREE DNA | Oncology, response to radiation, cell-free DNA, quantitative branched chain DNA amplification, plasma, reported as a radiation toxicity score |
| 56 | 3 | MoG | 0287U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score DNA and mRNA | Oncology (thyroid), DNA and mRNA, next generation sequencing analysis of 112 genes, fine needle aspirate or formalin fixed paraffinembedded (FFPE) tissue, algorithmic prediction of cancer recurrence, reported as a categorical risk result (low, intermediate, high) |
| 57 | 4 | MoG | 0288U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score DNA and mRNA | Oncology (lung), mRNA, quantitative PCR analysis of 11 genes (BAG1, BRCA1, CDC6, CDK2AP1, ERBB3, FUT3, IL11, LCK, RND3, SH3BGR, WNT3A) and 3 reference genes (ESD, TBP, YAP1), formalin-fixed paraffin-embedded (FFPE) tumor tissue, algorithmic interpretation reported as a recurrence risk score |
| 58 | 5 | MoG | 0289U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score mRNA | Neurology (Alzheimer disease), mRNA, gene expression profiling by RNA sequencing of 24 genes, whole blood, algorithm reported as predictive risk score |
| 59 | 6 | MoG | 0290U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score mRNA | Pain management, mRNA, gene expression profiling by RNA sequencing of 36 genes, whole blood, algorithm reported as predictive risk score |

| FACA Panel Item # | ALM Item # | Subcommittee | Code # | Code Type | Slide category | Long Code Descriptor |
|-------------------------|------------------|--------------|--------|-----------|---|---|
| 60 | 7 | MoG | 0291U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score mRNA | Psychiatry (mood disorders), mRNA, gene expression profiling by RNA sequencing of 144 genes, whole blood, algorithm reported as predictive risk score |
| 61 | 8 | MoG | 0292U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score mRNA | Psychiatry (stress disorders), mRNA, gene expression profiling by RNA sequencing of 72 genes, whole blood, algorithm reported as predictive risk score |
| 62 | 9 | MoG | 0293U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score mRNA | Psychiatry (suicidal ideation), mRNA, gene expression profiling by RNA sequencing of 54 genes, whole blood, algorithm reported as predictive risk score |
| 63 | 10 | MoG | 0294U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score mRNA | Longevity and mortality risk, mRNA, gene expression profiling by RNA sequencing of 18 genes, whole blood, algorithm reported as predictive risk score |
| 64 | 11 | СНІМ | 0295U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score PROTEINS | Oncology (breast ductal carcinoma in situ), protein expression profiling by immunohistochemistry of 7 proteins (COX2, FOXA1, HER2, Ki-67, p16, PR, SIAH2), with 4 clinicopathologic factors (size, age, margin status, palpability), utilizing formalin-fixed paraffin-embedded (FFPE) tissue, algorithm reported as a recurrence risk score |
| 65 | 24 | СНІМ | 0308U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score PROTEINS | Cardiology (coronary artery disease [CAD]), analysis of 3 proteins (high sensitivity [hs] troponin, adiponectin, and kidney injury molecule-1 [KIM-1]), plasma, algorithm reported as a risk score for obstructive CAD |
| 66 | 65 | MoG | 0329U | PLA | Genomic Sequencing Related Tests TARGETED: EXOME TRANSCRIPTOME, VARIANTS, REARRANGEMENTS, MICORSATELLITE INSTABILITY | Oncology (neoplasia), exome and transcriptome sequence analysis for sequence variants, gene copy number amplifications and deletions, gene rearrangements, microsatellite instability and tumor mutational burden utilizing DNA and RNA from tumor with DNA from normal blood or saliva for subtraction, report of clinically significant mutation(s) with therapy associations |
| 67 | 25 | СНІМ | 0309U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score PROTEINS | Cardiology (cardiovascular disease), analysis of 4 proteins (NT-proBNP, osteopontin, tissue inhibitor of metalloproteinase-1 [TIMP-1], and kidney injury molecule-1 [KIM-1]), plasma, algorithm reported as a risk score for major adverse cardiac event |
| 68 | 26 | СНІМ | 0310U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score PROTEINS | Pediatrics (vasculitis, Kawasaki disease [KD]), analysis of 3 biomarkers (NTproBNP, C-reactive protein, and T-uptake), plasma, algorithm reported as a risk score for D |

| FACA Panel Item # | ALM Item # | Subcommittee | Code # | Code Type | Slide category | Long Code Descriptor |
|-------------------------|------------------|--------------|--------|-----------------|--|--|
| 69 | 63 | MoG | 0327U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score CELL FREE DNA | Fetal aneuploidy (trisomy 13, 18, and 21), DNA sequence analysis of selected regions using maternal plasma, algorithm reported as a risk score for each trisomy, includes sex reporting, if performed |
| 70 | 33 | MoG | 0317U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score FISH | Oncology (lung cancer), four-probe FISH (3q29, 3p22.1, 10q22.3, 10cen) assay, whole blood, predictive algorithm generated evaluation reported as decreased or increased risk for lung cancer |
| 71 | 35 | MoG | 0319U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score RNA, SELECT TRANSCRIPTOME | Nephrology (renal transplant), RNA expression by select transcriptome sequencing, using pretransplant peripheral blood, algorithm reported as a risk score for early acute rejection |
| 72 | 36 | MoG | 0320U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score RNA, SELECT TRANSCRIPTOME | Nephrology (renal transplant), RNA expression by select transcriptome sequencing, using posttransplant peripheral blood, algorithm reported as a risk score for acute cellular rejection |
| 73 | 30 | MoG | 0314U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score mRNA | Oncology (cutaneous melanoma), mRNA gene expression profiling by RT-PCR of 35 genes (32 content and 3 housekeeping), utilizing formalin-fixed paraffin-embedded (FFPE) tissue, algorithm reported as a categorical result (ie, benign, intermediate, malignant) |
| 74 | 31 | MoG | 0315U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score mRNA | Oncology (cutaneous squamous cell carcinoma), mRNA gene expression profiling by RT-PCR of 40 genes (34 content and 6 housekeeping), utilizing formalin-fixed paraffin-embedded (FFPE) tissue, algorithm reported as a categorical risk result (ie, Class 1, Class 2A, Class 2B) |
| 75 | 12 | MoG | 0296U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score mRNA | Oncology (oral and/or oropharyngeal cancer), gene expression profiling by RNA sequencing at least 20 molecular features (eg, human and/or microbial mRNA), saliva, algorithm reported as positive or negative for signature associated with malignancy |
| 76 | 58 | MoG | 0245U | Reconsideration | Tests with algorithm in code descriptor to report risk/likelihood/predictive score DNA and RNA | Oncology (thyroid), mutation analysis of 10 genes and 37 RNA fusions and expression of 4 mRNA markers using next-generation sequencing, fine needle aspirate, report includes associated risk of malignancy expressed as a percentage) |
| 77 | 29 | MoG | 0313U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score DNA and RNA | Oncology (pancreas), DNA and mRNA next-generation sequencing analysis of 74 genes and analysis of CEA (CEACAM5) gene expression, pancreatic cyst fluid, algorithm reported as a categorical result (ie, negative, low probability of neoplasia or positive, high probability of neoplasia) |

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| 78 | 60 | MoG | 0324U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score TUMOR CELL GROWTH | Oncology (ovarian), spheroid cell culture, 4-drug panel (carboplatin, doxorubicin, gemcitabine, paclitaxel), tumor chemotherapy response prediction for each drug |
| 79 | 61 | MoG | 0325U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score | Oncology (ovarian), spheroid cell culture, poly (ADP-ribose) polymerase (PARP) inhibitors (niraparib, olaparib, rucaparib, velparib), tumor response prediction for each drug |
| 80 | 83 | MoG | 0X33U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score DNA | Oncology (pan-tumor), genetic profiling of 8 DNA-regulatory (epigenetic) markers by quantitative polymerase chain reaction (qPCR), whole blood, reported as a high or low probability of responding to immune checkpoint—inhibitor therapy |
| 81 | 84 | MoG | 0X34U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score CELL FREE DNA + PROTEINS | Oncology (liver), surveillance for hepatocellular carcinoma (HCC) in high-risk patients, analysis of methylation patterns on circulating cell-free DNA (cfDNA) plus measurement of serum of AFP/AFP-L3 and oncoprotein des-gamma-carboxy-prothrombin (DCP), algorithm reported as normal or abnormal result |
| 82 | 94 | MoG | 0X44U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score EXOSOME | Oncology (prostate), exosome-based analysis of 442 small noncoding RNAs (sncRNAs) by quantitative reverse transcription polymerase chain reaction (RT-qPCR), urine, reported as molecular evidence of no, low-, intermediate- or high- risk prostate of cancer |
| 83 | 38 | СНІМ | 0322U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score/ CHEMISTRY | Neurology (autism spectrum disorder [ASD]), quantitative measurements of 14 acyl carnitines and microbiome-derived metabolites, liquid chromatography with tandem mass spectrometry (LC-MS/MS), plasma, results reported as negative or positive for risk of metabolic subtypes associated with ASD |
| 84 | 64 | СНІМ | 0328U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score CHEMISTRY | Drug assay, definitive, 120 or more drugs and metabolites, urine, quantitative liquid chromatography with tandem mass spectrometry (LC-MS/MS), includes specimen validity and algorithmic analysis describing drug or metabolite and presence or absence of risks for a significant patient adverse event, per date of service |
| 85 | 102 | СНІМ | 0X53U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score PROTEIN | Infectious disease (bacterial or viral), biochemical assays, tumor necrosis factor-related apoptosis-inducing ligand (TRAIL), interferon gamma-induced protein-10 (IP-10), and C-reactive protein, serum, algorithm reported as likelihood of bacterial infection |
| 86 | 93 | СНІМ | 0X43U | PLA | Tests with algorithm in code descriptor to report risk/likelihood/predictive score ELECTROCHEMILUMINESCENT IMMUNOASSAY (ECLIA) | Oncology (pancreatic cancer), multiplex immunoassay of C5, C4, cystatin C, factor B, osteoprotegerin (OPG), gelsolin, IGFBP3, CA125 and multiplex electrochemiluminescent immunoassay (ECLIA) for CA19-9, serum, diagnostic algorithm reported qualitatively as positive, negative, or borderline |
| 87 | 28 | CHIM | 0312U | PLA | Immunology ELISA | Autoimmune diseases (eg, systemic lupus erythematosus [SLE]), analysis of 8 IgG autoantibodies and 2 cell-bound complement |

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| | | | | | | activation products using enzyme-linked immunosorbent immunoassay (ELISA), flow cytometry and indirect immunofluorescence, serum, or plasma and whole blood, individual components reported along with an algorithmic SLE-likelihood assessment |
| 88 | 42 | CHIM | 86015 | Reconsideration | Immunology IMMUNOASSAY | Actin (smooth muscle) antibody (ASMA), each |
| 89 | 43 | CHIM | 86036 | Reconsideration | Immunology IMMUNOASSAY FLUORESCENT | ANCA screen, each |
| 90 | 44 | CHIM | 86037 | Reconsideration | Immunology IMMUNOASSAY FLUORESCENT | ANCA titer |
| 91 | 45 | CHIM | 86051 | Reconsideration | Immunology ELISA | Aquaporin-4 (neuromyelitis optica [NMO]) antibody; enzyme-linked immunosorbent immunoassay (ELISA) |
| 92 | 46 | CHIM | 86052 | Reconsideration | Immunology IMMUNOFLUORESCENCE CELL-BASED | Aquaporin-4 (neuromyelitis optica [NMO]) antibody; cell-based immunofluorescence assay (CBA), each |
| 93 | 47 | CHIM | 86053 | Reconsideration | Immunology FLOW CYTOMETRY FLUORO CELL SORTING | Aquaporin-4, flow cytometry (ie, fluorescence-activated cell sorting [FACS]) |
| 94 | 48 | CHIM | 86231 | Reconsideration | Immunology IMMUNOFLUORESCENCE | Endomysial antibody |
| 95 | 49 | CHIM | 86258 | Reconsideration | Immunology ELISA | Gliadin (deamidated) (DGP) antibody |
| 98 | 52 | CHIM | 86364 | Reconsideration | Immunology ELISA | Tissue transglutaminase, each immunoglobulin |
| 96 | 50 | CHIM | 86362 | Reconsideration | Immunology IMMUNOFLUORESCENCE CELL-BASED | MOG IgG1, cell-based immunofluorescence assay |
| 97 | 51 | CHIM | 86363 | Reconsideration | Immunology FLOW CYTOMETRY FLUORO CELL SORTING | MOG IgG1, flow cytometry (ie, fluorescence-activated cell sorting [FACS] |
| 99 | 53 | CHIM | 86409 | Reconsideration | Immunology LUMINESCENCE CELL FUNCTION | Neutralizing antibody, severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]); titer |
| 100 | 54 | CHIM | 86413 | Reconsideration | Immunology IMMUNOASSAY | Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (Coronavirus disease [COVID-19]) antibody, quantitative |
| 101 | 55 | CHIM | 86596 | Reconsideration | Immunology IMMUNOASSAY (RIA) | Voltage gated calcium channel antibody, each |
| 103 | 87 | CHIM | 0X37U | PLA | Immunology | Oncology (plasma cell disorders and myeloma), circulating plasma cell immunologic selection, identification, morphological characterization, |

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| | | | | | IMMUNOMAGNETIC IMMUNOFLUORESCENT | and enumeration of plasma cells based on differential CD138, CD38, CD19, and CD45 protein biomarker expression, peripheral blood |
| 104 | 89 | MoG | 0X39U | PLA | Immunology IMMUNOMAGNETIC IMMUNOFLUORESCENT | Oncology (solid tumor), circulating tumor cell selection, identification, morphological characterization, detection and enumeration based on differential EpCAM, cytokeratins 8, 18, and 19, and CD45 protein biomarkers, and quantification of HER2 protein biomarker—expressing cells, peripheral blood |
| 105 | 105 | CHIM | 0X56U | PLA | Microbiology PANEL GENOMIC IDENTIFICATION | Human papilloma virus (HPV), high-risk types (ie, 16, 18, 31, 33, 45, 52 and 58) qualitative mRNA expression of E6/E7 by quantitative polymerase chain reaction (qPCR) |
| 102 | 56 | СНІМ | 87428 | Reconsideration | Microbiology IMMUNOMAGNETIC IMMUNOFLUORESCENT | Infectious agent antigen detection by immunoassay technique (eg, enzyme immunoassay [EIA], enzyme-linked immunosorbent assay [ELISA], fluorescence immunoassay [FIA], immunochemiluminometric assay [IMCA]), qualitative or semiquantitative; severe acute respiratory syndrome coronavirus (eg, SARS-CoV, SARS-CoV-2 [COVID-19]) and influenza virus types A and B |